



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

10/009,445B

Source:

IFW16

Date Processed by STIC:

10-12-04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission

User Manual - ePAVE)

2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450

3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):

U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/009,445B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino Numbering The numbering under each 5' amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing
- 6 PatentIn 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES" response to include the skipped sequences.
- 8 Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213> Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence.
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See: "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid.



IFW16

RAW SEQUENCE LISTING

DATE: 10/12/2004

PATENT APPLICATION: US/10/009,445B

TIME: 11:51:41

Input Set : D:\14094-20009.00 - Substitute Seqlist.txt

Output Set: N:\CRF4\10122004\J009445B.raw

4 <110> APPLICANT: BARCLAY, A. Neil
 5 BROWN, Marion H.
 6 GORMAN, Daniel M.
 7 LANIER, Lewis L.
 8 WRIGHT, Gavin J.
 9 CHERWINSKI, Holly
 10 PHILLIPS, Joseph H.
 11 HOEK, Robert M.
 12 SEDGWICK, Jonathan D.
 14 <120> TITLE OF INVENTION: OX2 RECEPTOR HOMOLOGS (AS AMENDED)
 16 <130> FILE REFERENCE: 140942000900
 18 <140> CURRENT APPLICATION NUMBER: US 10/009,445B
 19 <141> CURRENT FILING DATE: 2001-11-13
 21 <150> PRIOR APPLICATION NUMBER: PCT US00/12998
 22 <151> PRIOR FILING DATE: 2000-05-11
 24 <150> PRIOR APPLICATION NUMBER: GB 9925989.7
 25 <151> PRIOR FILING DATE: 1999-11-03
 28 <150> PRIOR APPLICATION NUMBER: GB 9911123.9
 29 <151> PRIOR FILING DATE: 1999-05-13
 31 <160> NUMBER OF SEQ ID NOS: 70
 33 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 36 <210> SEQ ID NO: 1
 37 <211> LENGTH: 1574
 38 <212> TYPE: DNA
 39 <213> ORGANISM: Unknown
 41 <220> FEATURE:
 42 <223> OTHER INFORMATION: Description of Unknown Organism: rodent; surmised
 43 rattus rattus
 45 <220> FEATURE:
 46 <221> NAME/KEY: CDS
 47 <222> LOCATION: (91)..(1071)
 49 <220> FEATURE:
 50 <221> NAME/KEY: mat_peptide
 51 <222> LOCATION: (162)..(1071)
 53 <400> SEQUENCE: 1
 54 agcggaggga tcttggtcat ggtcaccgct gctccctac ctgtgaagag aaagagcacc 60
 56 gagtgaagccg ctgaaaacca gaaaaccgaa atg ctc tgc ttt tgg aga act tct 114
 57 Met Leu Cys Phe Trp Arg Thr Ser
 58 -20
 60 cac gta gca gta ctc ttg atc tgg ggg gtc ttc gcg gct gag tca agt 162
 61 His Val Ala Val Leu Leu Ile Trp Gly Val Phe Ala Ala Glu Ser Ser
 62 -15 -10 -5 -1
 64 tgt cct gat aag aat caa aca atg cag aac aat tca tca act atg aca 210

(pg. 6-7)
 Does Not Comply
 Corrected Diskette Needed
 (pg. 3, 6)

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DATE: 10/12/2004

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TIME: 11:51:41

Input Set : D:\14094-20009.00 - Substitute Seqlist.txt

Output Set: N:\CRF4\10122004\J009445B.raw

65	Cys	Pro	Asp	Lys	Asn	Gln	Thr	Met	Gln	Asn	Asn	Ser	Ser	Thr	Met	Thr	
66	1				5				10					15			
68	gaa	gtt	aac	act	aca	gtg	ttt	gta	cag	atg	ggg	aaa	aag	gct	ctg	ctc	258
69	Glu	Val	Asn	Thr	Thr	Val	Phe	Val	Gln	Met	Gly	Lys	Lys	Ala	Leu	Leu	
70				20				25						30			
72	tgc	tgc	cct	tct	att	tca	ctg	aca	aaa	gta	ata	tta	ata	aca	tgg	aca	306
73	Cys	Cys	Pro	Ser	Ile	Ser	Leu	Thr	Lys	Val	Ile	Leu	Ile	Thr	Trp	Thr	
74			35					40					45				
76	ata	acc	ctc	aga	gga	cag	cct	tcc	tgc	ata	ata	tcc	tac	aaa	gca	gac	354
77	Ile	Thr	Leu	Arg	Gly	Gln	Pro	Ser	Cys	Ile	Ile	Ser	Tyr	Lys	Ala	Asp	
78		50					55					60					
80	aca	agg	gag	acc	cat	gaa	agc	aac	tgc	tcg	gac	aga	agc	atc	acc	tgg	402
81	Thr	Arg	Glu	Thr	His	Glu	Ser	Asn	Cys	Ser	Asp	Arg	Ser	Ile	Thr	Trp	
82	65					70				75					80		
84	gcc	tcc	aca	cct	gac	ctc	gct	cct	gac	ctt	cag	atc	agt	gca	gtg	gcc	450
85	Ala	Ser	Thr	Pro	Asp	Leu	Ala	Pro	Asp	Leu	Gln	Ile	Ser	Ala	Val	Ala	
86				85				90					95				
88	ctc	cag	cat	gaa	ggg	cgt	tac	tca	tgt	gat	ata	gca	gta	cct	gac	ggg	498
89	Leu	Gln	His	Glu	Gly	Arg	Tyr	Ser	Cys	Asp	Ile	Ala	Val	Pro	Asp	Gly	
90			100					105					110				
92	aat	ttc	caa	aac	atc	tat	gac	ctc	caa	gtg	ctg	gtg	ccc	cct	gaa	gta	546
93	Asn	Phe	Gln	Asn	Ile	Tyr	Asp	Leu	Gln	Val	Leu	Val	Pro	Pro	Glu	Val	
94			115					120					125				
96	acc	cac	ttt	cca	ggg	gaa	aat	aga	act	gca	gtt	tgt	gag	gcg	att	gca	594
97	Thr	His	Phe	Pro	Gly	Glu	Asn	Arg	Thr	Ala	Val	Cys	Glu	Ala	Ile	Ala	
98		130					135					140					
100	ggc	aaa	cct	gct	gcg	cag	atc	tct	tgg	acg	cca	gat	ggg	gat	tgt	gtc	642
101	Gly	Lys	Pro	Ala	Ala	Gln	Ile	Ser	Trp	Thr	Pro	Asp	Gly	Asp	Cys	Val	
102	145					150					155				160		
104	gct	aag	aat	gaa	tca	cac	agc	aat	ggc	acc	gtg	act	gtc	cgg	agc	aca	690
105	Ala	Lys	Asn	Glu	Ser	His	Ser	Asn	Gly	Thr	Val	Thr	Val	Arg	Ser	Thr	
106				165					170				175				
108	tgc	cac	tgg	gag	cag	agc	cac	gtg	tct	gtc	gtg	ttc	tgt	gtt	gtc	tct	738
109	Cys	His	Trp	Glu	Gln	Ser	His	Val	Ser	Val	Val	Phe	Cys	Val	Val	Ser	
110			180					185					190				
112	cac	ttg	aca	act	ggg	aac	cag	tct	ctg	tct	ata	gaa	ctg	ggg	aga	ggg	786
113	His	Leu	Thr	Thr	Gly	Asn	Gln	Ser	Leu	Ser	Ile	Glu	Leu	Gly	Arg	Gly	
114			195					200					205				
116	ggg	gac	caa	tta	tta	gga	tca	tac	att	caa	tac	atc	atc	cca	tct	att	834
117	Gly	Asp	Gln	Leu	Leu	Gly	Ser	Tyr	Ile	Gln	Tyr	Ile	Ile	Pro	Ser	Ile	
118		210					215					220					
120	att	att	ttg	atc	atc	ata	gga	tgc	att	tgt	ctt	ttg	aaa	atc	agt	ggc	882
121	Ile	Ile	Leu	Ile	Ile	Ile	Gly	Cys	Ile	Cys	Leu	Leu	Lys	Ile	Ser	Gly	
122	225					230					235				240		
124	tgc	aga	aaa	tgt	aaa	ttg	cca	aaa	tcg	gga	gct	act	cca	gat	att	gag	930
125	Cys	Arg	Lys	Cys	Lys	Leu	Pro	Lys	Ser	Gly	Ala	Thr	Pro	Asp	Ile	Glu	
126				245					250				255				
128	gag	gat	gaa	atg	cag	ccg	tat	gct	agc	tac	aca	gag	aag	agc	aat	cca	978
129	Glu	Asp	Glu	Met	Gln	Pro	Tyr	Ala	Ser	Tyr	Thr	Glu	Lys	Ser	Asn	Pro	

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Input Set : D:\14094-20009.00 - Substitute Seqlist.txt

Output Set: N:\CRF4\10122004\J009445B.raw

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130          260          265          270
132 ctc tat gat act gtg acc acg acg gag gca cac cca gcg tca caa ggc 1026
133 Leu Tyr Asp Thr Val Thr Thr Thr Glu Ala His Pro Ala Ser Gln Gly
134          275          280          285
136 aaa gtc aat ggc aca gac tgt ctt act ttg tca gcc atg gga atc 1071
137 Lys Val Asn Gly Thr Asp Cys Leu Thr Leu Ser Ala Met Gly Ile
138          290          295          300
140 tagaaccaag gaaaagaagt caagagacat cataattact gcttttcttt ctttaaactt 1131
142 ctccaatgga gggaaattag ctcttctgaa gttcttagaa agcaciaatg ttctaattga 1191
144 ttgaccttta agttcttcta tcattggaag ttggaatct ttgctgtac ctgttaattc 1251
146 taggaagaac tgatttaatt attacaaaga aagcacattg ttatggtaaa atatcaaatt 1311
148 gtgcaataca atgatgaaaa ctgagtttcc tcaagaaata actgcagaag gaacaatcat 1371
150 tactaaagca tttcatgtga gttcttccaa aaaagaaaa cctgtgtat acgacatgat 1431
152 tatggtatgt gtgtgccttt atatgtttgt ttacaaatgt gtatatatgc acacatctga 1491
154 ttatcaagac atctctgtca aaaactcact ggcgttcag atttatgaaa gctaataaag 1551
156 tgagtattgg agatgttttt ata 1574
159 <210> SEQ ID NO: 2
160 <211> LENGTH: 327
161 <212> TYPE: PRT
162 <213> ORGANISM: Unknown
W--> 164 <220> FEATURE:
W--> 164 <223> OTHER INFORMATION:
W--> 164 <400> 2
165 Met Leu Cys Phe Trp Arg Thr Ser His Val Ala Val Leu Leu Ile Trp
166          -20          -15          -10
168 Gly Val Phe Ala Ala Glu Ser Ser Cys Pro Asp Lys Asn Gln Thr Met
169          -5          -1 1 5
171 Gln Asn Asn Ser Ser Thr Met Thr Glu Val Asn Thr Thr Val Phe Val
172          10          15          20
174 Gln Met Gly Lys Lys Ala Leu Leu Cys Cys Pro Ser Ile Ser Leu Thr
175 25          30          35          40
177 Lys Val Ile Leu Ile Thr Trp Thr Ile Thr Leu Arg Gly Gln Pro Ser
178          45          50          55
180 Cys Ile Ile Ser Tyr Lys Ala Asp Thr Arg Glu Thr His Glu Ser Asn
181          60          65          70
183 Cys Ser Asp Arg Ser Ile Thr Trp Ala Ser Thr Pro Asp Leu Ala Pro
184          75          80          85
187 Asp Leu Gln Ile Ser Ala Val Ala Leu Gln His Glu Gly Arg Tyr Ser
188          90          95          100
190 Cys Asp Ile Ala Val Pro Asp Gly Asn Phe Gln Asn Ile Tyr Asp Leu
191 105          110          115          120
193 Gln Val Leu Val Pro Pro Glu Val Thr His Phe Pro Gly Glu Asn Arg
194          125          130          135
196 Thr Ala Val Cys Glu Ala Ile Ala Gly Lys Pro Ala Ala Gln Ile Ser
197          140          145          150
199 Trp Thr Pro Asp Gly Asp Cys Val Ala Lys Asn Glu Ser His Ser Asn
200          155          160          165
202 Gly Thr Val Thr Val Arg Ser Thr Cys His Trp Glu Gln Ser His Val
203          170          175          180

```

Pls see error explanation on page 8. ↓

Pls insert, whenever <213> response is artificial Unknown or Genus/Species.

↑
The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING

DATE: 10/12/2004

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TIME: 11:51:41

Input Set : D:\14094-20009.00 - Substitute Seqlist.txt

Output Set: N:\CRF4\10122004\J009445B.raw

```

205 Ser Val Val Phe Cys Val Val Ser His Leu Thr Thr Gly Asn Gln Ser
206 185          190          195          200
208 Leu Ser Ile Glu Leu Gly Arg Gly Gly Asp Gln Leu Leu Gly Ser Tyr
209          205          210          215
211 Ile Gln Tyr Ile Ile Pro Ser Ile Ile Ile Leu Ile Ile Ile Gly Cys
212          220          225          230
214 Ile Cys Leu Leu Lys Ile Ser Gly Cys Arg Lys Cys Lys Leu Pro Lys
215          235          240          245
217 Ser Gly Ala Thr Pro Asp Ile Glu Glu Asp Glu Met Gln Pro Tyr Ala
218          250          255          260
220 Ser Tyr Thr Glu Lys Ser Asn Pro Leu Tyr Asp Thr Val Thr Thr Thr
221 265          270          275          280
223 Glu Ala His Pro Ala Ser Gln Gly Lys Val Asn Gly Thr Asp Cys Leu
224          285          290          295
226 Thr Leu Ser Ala Met Gly Ile
227          300
230 <210> SEQ ID NO: 3
231 <211> LENGTH: 1604
232 <212> TYPE: DNA
233 <213> ORGANISM: Unknown
235 <220> FEATURE:
236 <223> OTHER INFORMATION: Description of Unknown Organism:primate; surmised
237      homo sapiens
239 <220> FEATURE:
240 <221> NAME/KEY: CDS
241 <222> LOCATION: (217)..(1101)
243 <220> FEATURE:
244 <221> NAME/KEY: mat_peptide
245 <222> LOCATION: (295)..(1101)
247 <400> SEQUENCE: 3
248 cagagaaaag cttctgttcg tccaagttac taaccaggct aaaccacata gacgtgaagg 60
250 aaggggctag aaggaagga gtgcccact gttgatggg taagaggatc ctgtactgag 120
252 aagttgacca gagagggtct caccatgcgc acagttcctt ctgtaccagt gtggaggaaa 180
254 agtactgagt gaagggcaga aaaagagaaa acagaa atg ctc tgc cct tgg aga 234
255          Met Leu Cys Pro Trp Arg
256          -25
258 act gct aac cta ggg cta ctg ttg att ttg act atc ttc tta gtg gcc 282
259 Thr Ala Asn Leu Gly Leu Leu Leu Ile Leu Thr Ile Phe Leu Val Ala
260 -20          -15          -10          -5
262 gaa gcg gag ggt gct gct caa cca aac aac tca tta atg ctg caa act 330
263 Glu Ala Glu Gly Ala Ala Gln Pro Asn Asn Ser Leu Met Leu Gln Thr
264          -1 1          5          10
266 agc aag gag aat cat gct tta gct tca agc agt tta tgt atg gat gaa 378
267 Ser Lys Glu Asn His Ala Leu Ala Ser Ser Ser Leu Cys Met Asp Glu
268          15          20          25
270 aaa cag att aca cag aac tac tcg aaa gta ctc gca gaa gtt aac act 426
271 Lys Gln Ile Thr Gln Asn Tyr Ser Lys Val Leu Ala Glu Val Asn Thr
272          30          35          40
274 tca tgg cct gta aag atg gct aca aat gct gtg ctt tgt tgc cct cct 474

```

RAW SEQUENCE LISTING

DATE: 10/12/2004

PATENT APPLICATION: US/10/009,445B

TIME: 11:51:41

Input Set : D:\14094-20009.00 - Substitute Seqlist.txt

Output Set: N:\CRF4\10122004\J009445B.raw

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275 Ser Trp Pro Val Lys Met Ala Thr Asn Ala Val Leu Cys Cys Pro Pro
276 45 50 55 60
278 atc gca tta aga aat ttg atc ata ata aca tgg gaa ata atc ctg aga 522
279 Ile Ala Leu Arg Asn Leu Ile Ile Ile Thr Trp Glu Ile Ile Leu Arg
280 65 70 75
282 ggc cag cct tcc tgc aca aaa gcc tac aag aaa gaa aca aat gag acc 570
283 Gly Gln Pro Ser Cys Thr Lys Ala Tyr Lys Lys Glu Thr Asn Glu Thr
284 80 85 90
286 aag gaa acc aac tgt act gat gag aga ata acc tgg gtc tcc aga cct 618
287 Lys Glu Thr Asn Cys Thr Asp Glu Arg Ile Thr Trp Val Ser Arg Pro
288 95 100 105
290 gat cag aat tcg gac ctt cag att cgt acc gtg gcc atc act cat gac 666
291 Asp Gln Asn Ser Asp Leu Gln Ile Arg Thr Val Ala Ile Thr His Asp
292 110 115 120
294 ggg tat tac aga tgc ata atg gta aca cct gat ggg aat ttc cat cgt 714
295 Gly Tyr Tyr Arg Cys Ile Met Val Thr Pro Asp Gly Asn Phe His Arg
296 125 130 135 140
298 gga tat cac ctc caa gtg tta gtt aca cct gaa gtg acc ctg ttt caa 762
299 Gly Tyr His Leu Gln Val Leu Val Thr Pro Glu Val Thr Leu Phe Gln
300 145 150 155
302 aac agg aat aga act gca gta tgc aag gca gtt gca ggg aag cca gct 810
303 Asn Arg Asn Arg Thr Ala Val Cys Lys Ala Val Ala Gly Lys Pro Ala
304 160 165 170
306 gcg cat atc tcc tgg atc cca gag ggc gat tgt gcc act aag caa gaa 858
307 Ala His Ile Ser Trp Ile Pro Glu Gly Asp Cys Ala Thr Lys Gln Glu
308 175 180 185
310 tac tgg agc aat ggc aca gtg act gtt aag agt aca tgc cac tgg gag 906
311 Tyr Trp Ser Asn Gly Thr Val Thr Val Lys Ser Thr Cys His Trp Glu
312 190 195 200
314 gtc cac aat gtg tct acc gtg acc tgc cac gtc tcc cat ttg act ggc 954
315 Val His Asn Val Ser Thr Val Thr Cys His Val Ser His Leu Thr Gly
316 205 210 215 220
318 aac aag agt ctg tac ata gag cta ctt cct gtt cca ggt gcc aaa aaa 1002
319 Asn Lys Ser Leu Tyr Ile Glu Leu Leu Pro Val Pro Gly Ala Lys Lys
320 225 230 235
322 atc agc aaa att ata tat tcc ata tat cat cct tac tat tat tat tta 1050
323 Ile Ser Lys Ile Ile Tyr Ser Ile Tyr His Pro Tyr Tyr Tyr Tyr Leu
324 240 245 250
326 gac cat cgt ggg att cat ttg gtt gtt gaa agt caa tgg ctg cag aaa 1098
327 Asp His Arg Gly Ile His Leu Val Val Glu Ser Gln Trp Leu Gln Lys
328 255 260 265
330 ata taaattgaat aaaacagaat ctactccagt tgttgaggag gatgaaatgc 1151
331 Ile
333 agccctatgc cagctacaca gagaagaaca atcctctcta tgatactaca aacaaggtga 1211
335 aggcattctga ggcattacaa agtgaagttg acacagacct ccatacttta taagttgttg 1271
337 gactctagta ccaagaaaca acaacaaacg agatacatta taattactgt ctgattttct 1331
339 tacagttcta gaatgaagac ttatattgaa attaggtttt ccaaggttct tagaagacat 1391
341 tttaatggat tctcattcat acccttgtat aattggaatt tttgattctt agctgctacc 1451
343 agctagttct ctgaagaact gatgttatta caaagaaaat acatgcccac gaccaaatat 1511

```

<210> 21

<211> 1044

<212> DNA

<213> reverse translation

<220>

<221> misc_feature

<222> (1)..(1044)

<223> n may be a, c, g, or t

<400> 21

Invalid
Response

Mandatory, <213>
Responses has to be
either artificial/
Unknown or Genus/
Species. Pls see
item # 10 on
error summary
Sheet.

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 10/12/2004
PATENT APPLICATION: US/10/009,445B TIME: 11:51:42

Input Set : D:\14094-20009.00 - Substitute Seqlist.txt
Output Set: N:\CRF4\10122004\J009445B.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:13; N Pos. 6,18,21,24,30,33,36,39,42,51,54,60,63,69,72,78,93,108,111
Seq#:13; N Pos. 114,120,126,132,135,138,144,153,162,165,168,177,180,186,189
Seq#:13; N Pos. 192,198,204,210,216,222,225,228,231,237,240,252,261,267,270
Seq#:13; N Pos. 276,285,294,300,303,309,315,318,321,324,330,333,336,342,351
Seq#:13; N Pos. 354,357,360,363,375,378,384,396,399,402,408,432,438,441,444
Seq#:13; N Pos. 447,450,456,459,468,471,480,483,486,489,498,504,507,513,516
Seq#:13; N Pos. 519,528,534,537,543,552,555,567,573,579,582,585,588,591,594
Seq#:13; N Pos. 597,600,618,624,627,630,633,642,645,648,654,657,660,663,672
Seq#:13; N Pos. 675,678,687,690,693,696,699,708,711,714,717,738,741,753,765
Seq#:13; N Pos. 777,780,789,792,798,810,813,819,822,825,828,831,858,864,867
Seq#:13; N Pos. 873,882,888,891,900,903,906,909,912,918,924,927,930,936,942
Seq#:13; N Pos. 948,951,960,963,966,969,972,978
Seq#:14; N Pos. 6,12,18,21,24,30,33,36,39,42,48,51,60,63,66,72,78,81,84,90
Seq#:14; N Pos. 99,102,108,114,117,132,135,138,141,144,147,150,174,186,192
Seq#:14; N Pos. 195,198,204,210,213,219,222,231,234,240,243,246,255,258,264
Seq#:14; N Pos. 267,270,276,288,303,306,309,315,318,324,330,345,354,363,372
Seq#:14; N Pos. 381,387,393,396,399,402,414,420,429,432,435,438,444,453,462
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Seq#:14; N Pos. 552,558,561,564,567,576,579,582,585,591,594,597,606,615,621
Seq#:14; N Pos. 630,633,651,657,660,663,666,669,675,678,693,702,705,708,711
Seq#:14; N Pos. 714,723,726,732,735,738,747,750,762,765,768,771,774,777,780
Seq#:14; N Pos. 792,807,819,834,843,846,855,858,861,867,876
Seq#:15; N Pos. 18,21,24,27,30,33,36,39,42,51,54,60,63,66,69,72,78,93,96
Seq#:15; N Pos. 108,111,114,117,120,123,129,135,138,141,144,147,156,159,165
Seq#:15; N Pos. 168,171,183,189,192,195,201,204,207,213,228,231,234,237,240
Seq#:15; N Pos. 243,249,255,264,270,276,285,288,294,297,300,309,315,318,321
Seq#:15; N Pos. 324,333,336,342,351,354,357,360,363,375,378,384,393,396,399
Seq#:15; N Pos. 402,408,432,438,441,444,447,450,456,459,468,480,483,486,489
Seq#:15; N Pos. 498,504,507,513,516,519,528,534,537,543,552,555,558,561,567
Seq#:15; N Pos. 573,579,582,585,588,591,594,597,600,624,627,633,636,645,648
Seq#:15; N Pos. 654,657,660,669,672,675,684,687,690,693,696,705,708,711,714
Seq#:15; N Pos. 723,735,738,750,762,774,777,786,789,795,807,810,816,822,825
Seq#:15; N Pos. 828,831,855,861,864,870,879,885,888,897,900,903,909,915,921
Seq#:15; N Pos. 924,927,933,939,945,948,957,960,963,966,969,975
Seq#:16; N Pos. 6,9,21,33,36,45,51,60,66,69,72,87,90,93,102,105,111,114,117
Seq#:16; N Pos. 123,135,150,153,156,162,165,171,177,192,201,210,219,222,228
Seq#:16; N Pos. 234,240,243,246,249,261,267,276,279,282,288,291,300,309,312
Seq#:16; N Pos. 318,321,324,327,333,345,348,357,363,366,369,372,375,381,387
Seq#:16; N Pos. 396,399,408,411,414,423,426,429,432,438,441,444,453,462,468
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Seq#:16; N Pos. 555,558,561,570,573,579,582,585,594,597,600,603,609,615,618
Seq#:16; N Pos. 621,624,627,630,633,636,639,642,645,648,651,654,663,669,675
Seq#:16; N Pos. 678,681,687,690,696,699,702,705,708,714,726,738,741,747,750
Seq#:17; N Pos. 3,6,12,15,27,36,42,51,60,66,69,72,81,87,90,93,96,108,114

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 10/12/2004
PATENT APPLICATION: US/10/009,445B TIME: 11:51:42

Input Set : D:\14094-20009.00 - Substitute Seqlist.txt
Output Set: N:\CRF4\10122004\J009445B.raw

Seq#:17; N Pos. 123,126,129,132,135,147,156,168,171,174,180,195,204,210,213
Seq#:17; N Pos. 216,219,222,228,231,240,243,252,255,258,261,270,276,279,285
Seq#:17; N Pos. 288,291,300,306,309,315,324,327,333,339,345,351,354,357,360
Seq#:17; N Pos. 363,366,369,372,396,399,402,405,408,417,420,426,429,432,441
Seq#:17; N Pos. 444,447,456,459,462,465,468,471,474,477,480,483,486,489,492
Seq#:17; N Pos. 495,501,507,516,519,522,525,534,537,543,546,552,567,573,576
Seq#:17; N Pos. 579,582

Use of <220> Feature (NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"
or "Unknown". Please explain source of genetic material in <220> to <223>
section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32)
(Sec.1.823 of new Rules)

Seq#:2,4,6,8,10,12,20,23

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/009,445B

DATE: 10/12/2004

TIME: 11:51:42

Input Set : D:\14094-20009.00 - Substitute Seqlist.txt

Output Set: N:\CRF4\10122004\J009445B.raw

L:164 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:2, <213>
ORGANISM:Unknown

L:164 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:2, <213>
ORGANISM:Unknown

L:164 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:164

L:355 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:4, <213>
ORGANISM:Unknown

L:355 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:4, <213>
ORGANISM:Unknown

L:355 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:355

L:541 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:6, <213>
ORGANISM:Unknown

L:541 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:6, <213>
ORGANISM:Unknown

L:541 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:541

L:699 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:8, <213>
ORGANISM:Unknown

L:699 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:8, <213>
ORGANISM:Unknown

L:699 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:699

L:836 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:10, <213>
ORGANISM:Unknown

L:836 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:10, <213>
ORGANISM:Unknown

L:836 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:836

L:992 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:12, <213>
ORGANISM:Unknown

L:992 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:12, <213>
ORGANISM:Unknown

L:992 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:12,Line#:992

L:1059 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
M:341 Repeated in SeqNo=13

L:1105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
M:341 Repeated in SeqNo=14

L:1147 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
M:341 Repeated in SeqNo=15

L:1193 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
M:341 Repeated in SeqNo=16

L:1231 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
M:341 Repeated in SeqNo=17

L:1263 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
M:341 Repeated in SeqNo=18

L:1405 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:20, <213>
ORGANISM:Unknown

L:1405 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:20, <213>
ORGANISM:Unknown

L:1405 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:20,Line#:1405

L:1484 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0
M:341 Repeated in SeqNo=21

L:1614 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:23, <213>
ORGANISM:Unknown

L:1614 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:23, <213>
ORGANISM:Unknown

L:1614 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:23,Line#:1614
L:1678 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0
M:341 Repeated in SeqNo=24